

re-run

IFW16

RAW SEQUENCE LISTING

DATE: 08/23/2004

PATENT APPLICATION: US/10/051,902A

TIME: 09:11:44

Input Set : N:\AMC\US10051902A.raw

Output Set: N:\CRF4\08232004\J051902A.raw

1 <110> APPLICANT: Allen, Stephen M.
 2 Hitz, William D.
 3 Kinney, Anthony J.
 4 <120> TITLE OF INVENTION: Plant Sugar Transport Proteins
 5 <130> FILE REFERENCE: BB1163USDIV
 --> 6 <140> CURRENT APPLICATION NUMBER: US/10/051,902A
 7 <141> CURRENT FILING DATE: 2002-01-17
 8 <150> PRIOR APPLICATION NUMBER: 60/083,044
 9 <151> PRIOR FILING DATE: 1998-04-24
 10 <160> NUMBER OF SEQ ID NOS: 30
 11 <170> SOFTWARE: Microsoft Office 97
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2824
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Zea mays
 17 <220> FEATURE:
 18 <221> NAME/KEY: unsure
 19 <222> LOCATION: (29)
 20 <223> OTHER INFORMATION: n = a, c, g or t
 21 <220> FEATURE:
 22 <221> NAME/KEY: unsure
 23 <222> LOCATION: (622)
 24 <223> OTHER INFORMATION: n = a, c, g or t
 25 <220> FEATURE:
 26 <221> NAME/KEY: unsure
 27 <222> LOCATION: (636)
 28 <223> OTHER INFORMATION: n = a, c, g or t
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 30 <221> NAME/KEY: unsure
 31 <222> LOCATION: (638)
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 33 <220> FEATURE:
 34 <221> NAME/KEY: unsure
 35 <222> LOCATION: (669)
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 37 <220> FEATURE:
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 39 <222> LOCATION: (771)
 40 <223> OTHER INFORMATION: n = a, c, g or t
 41 <220> FEATURE:
 42 <221> NAME/KEY: unsure
 43 <222> LOCATION: (822)
 44 <223> OTHER INFORMATION: n = a, c, g or t

*p.6*

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45 <220> FEATURE:
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47 <222> LOCATION: (856)
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52 <223> OTHER INFORMATION: n = a, c, g or t
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54 <221> NAME/KEY: unsure
55 <222> LOCATION: (896)
56 <223> OTHER INFORMATION: n = a, c, g or t
57 <220> FEATURE:
58 <221> NAME/KEY: unsure
59 <222> LOCATION: (944)
60 <223> OTHER INFORMATION: n = a, c, g or t
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63      tccgcacccc tcgctctcca accccaacgc gcggcgcttg taaaattcac ctccagcgct 120
64      actccagttt ggccacctca ccaccgcgcg ccgctgttta agaaggcccc gcgcccgcgc 180
65      ggggatcacg aaccttgccc gccgctgccg gagggtgggc gtagatttcc ggcgcccatg 240
66      gggggcgccg tgatggtcgc catcgcgccc tctatcgcca acttgctgca gggctgggac 300
67      aatgcgacaa ttgctggagc cgctcctgtac ataaagaagg aattcaacct gcagagcgag 360
68      cctctgatcg aaggcctcat cgctcgccatg ttctcattg gggcaacagt catcacaaca 420
69      tctccggggc caagggtga ctgcgttggt aggaggccca tgctggtcgc ctcggtgtgc 480
70      ctctacttcg tcagtgggct ggtgatgctt tgggcgcca ttgtgtacat cttgctcctc 540
71      gcaaggctca ttgatgggtt cgggtatcgg ttggcggtca cactgttcc tctctacatc 600
72      tccgaaactg caccgcacag anattcttg ggctgntnga acacgttgcc gcagttcatt 660
73      ggggtcagng gagggatgtt cctctcctac tgcattggtt ttgggatgtc cctcatgccc 720
74      aaacctgatt ggaggctcat gcttgaggtt ctgctgatcc cgtcacttat ntactttgga 780
75      ctgactgtct tctacttgcc tgaatcacca aggtggcttg tnagcaaagg aaggatggcg 840
76      gaggcgaaga gaggntgca aaggctgcgg ggaagagaag atgtctcang ggaganggct 900
77      cttctagttg aaggtttggg ggtcggtaaa gatacacgta ttnagagta catcattgga 960
78      cctgccaccg aggcagccga tgatcttgta actgacggtg ataaggaaca aatcacactt 1020
79      tatgggcctg aagaaggcca gtcattggatt gctcgacctt ctaagggacc catcatgctt 1080
80      ggaagtgtgc tttctcttgc atctcgctcat gggagcatgg tgaaccagag tgtaccctt 1140
81      atggatccga ttgtgacact ttttggtagt gtccatgaga atatgectca agctggagga 1200
82      agtatgagga gcacattgtt tccaaacttt ggaagtatgt tcagtgtcac agatcagcat 1260
83      gccaaaaatg agcagtggga tgaagagaat cttcataggg atgacgagga gtacgcatct 1320
84      gatggtgcag gaggtgacta tgaggacaat ctccatagcc cattgctgtc caggcaggca 1380
85      acaggtgcgg aagggaagga cattgtgcac catggtcacc gtggaagtgc tttgagcatg 1440
86      agaaggcaaa gcctcttagg ggaggggtgga gatggtgtga gcagcactga tatcggtggg 1500
87      ggatggcagc ttgcttgga atggtcagag aagggaagtg agaatggtag aaaggaaggt 1560
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90      ttagtaagtc agtcagcact tttctcaaaagggtctgtg aaccacgcat gtcagatgct 1740
91      gccatggttc acccatctga ggtagctgcc aaaggttcac gttggaaaga tttgtttgaa 1800
92      cctggagtga ggctgcccgt gttagtcggt gttggaattc agatccttca acagtttgct 1860
93      ggaataaacg gtgttctgta ctatacccca caaattcttg agcaagctgg tgtggcagtt 1920

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94      attctttcca aatttggctc cagctcggca tcagcatcca tcttgatcag ttctctcact 1980
95      accttactaa tgcttccttg cattggcttt gccatgctgc ttatggatct ttccggaaga 2040
96      aggtttttgc tgctaggcac aattccaatc ttgatagcat ctctagttat cctggttgtg 2100
97      tccaatctaa ttgatttggg tacactagcc catgctttgc tctccaccat cagtgttatc 2160
98      gtctacttct gctgcttcgt tatgggattt ggtcccatcc ccaacatttt atgtgcagag 2220
99      atctttccaa ccagggttcg tggcctctgt attgccattt gtgcctttac attctggatc 2280
100     ggagatatca tcgtcaccta cagccttctt gtgatgctga atgctattgg actggcgggt 2340
101     gttttcagca tatatgcagt cgtatgcttg atttcctttg tgttcgtctt ccttaagggtc 2400
102     cctgagacaa aggggatgcc ccttgagggtt attaccgaat tctttgcagt tgggtgcgaag 2460
103     caageggctg caaaagccta atttcttttg tacctttgtg tgcaactatt gcactgtaag 2520
104     ttagaaactt gaaggggttt caccaagaag ctcgagaaat tactttggat ttgtgtaaag 2580
105     gttaagggaa cgaacatctg ctcatgctcc tcaaacggta aaaaagagtc cctcaatggc 2640
106     aaataggagt cgtaagtgtg tcaatgtcat ttaccatatg ttttacctat ttgtactgta 2700
107     ttataagtca agctattcaa cgctggttgt tgctagaaat ctttagaaca aagatgataa 2760
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109     aaaa
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112 <211> LENGTH: 747
113 <212> TYPE: PRT
114 <213> ORGANISM: Zea mays
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116 <221> NAME/KEY: UNSURE
117 <222> LOCATION: (129)
118 <223> OTHER INFORMATION: Xaa = any amino acid
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120 <221> NAME/KEY: UNSURE
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126 <223> OTHER INFORMATION: Xaa = any amino acid
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129 <222> LOCATION: (178)
130 <223> OTHER INFORMATION: Xaa = any amino acid
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141 <222> LOCATION: (220)
142 <223> OTHER INFORMATION: Xaa = any amino acid
143 <220> FEATURE:

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144 <221> NAME/KEY: UNSURE
145 <222> LOCATION: (236)
146 <223> OTHER INFORMATION: Xaa = any amino acid
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149      1          5          10          15
150 Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
151      20          25          30
152 Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
153      35          40          45
154 Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly
155      50          55          60
156 Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala
157      65          70          75          80
158 Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val
159      85          90          95
160 Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu
161      100         105         110
162 Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro His Arg
163      115         120         125
W--> 164 Xaa Ser Trp Gly Xaa Xaa Asn Thr Leu Pro Gln Phe Ile Gly Val Xaa
165      130         135         140
166 Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met
167      145         150         155         160
168 Pro Lys Pro Asp Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser
169      165         170         175
170 Leu Xaa Tyr Phe Gly Leu Thr Val Phe Tyr Leu Pro Glu Ser Pro Arg
171      180         185         190
172 Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Xaa Gln
173      195         200         205
174 Arg Leu Arg Gly Arg Glu Asp Val Ser Xaa Glu Xaa Ala Leu Leu Val
175      210         215         220
176 Glu Gly Leu Gly Val Gly Lys Asp Thr Arg Ile Xaa Glu Tyr Ile Ile
177      225         230         235         240
178 Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val Thr Asp Gly Asp Lys
179      245         250         255
180 Glu Gln Ile Thr Leu Tyr Gly Pro Glu Glu Gly Gln Ser Trp Ile Ala
181      260         265         270
182 Arg Pro Ser Lys Gly Pro Ile Met Leu Gly Ser Val Leu Ser Leu Ala
183      275         280         285
184 Ser Arg His Gly Ser Met Val Asn Gln Ser Val Pro Leu Met Asp Pro
185      290         295         300
186 Ile Val Thr Leu Phe Gly Ser Val His Glu Asn Met Pro Gln Ala Gly
187      305         310         315         320
188 Gly Ser Met Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser
189      325         330         335
190 Val Thr Asp Gln His Ala Lys Asn Glu Gln Trp Asp Glu Glu Asn Leu
191      340         345         350
192 His Arg Asp Asp Glu Glu Tyr Ala Ser Asp Gly Ala Gly Gly Asp Tyr

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193																
194	Glu	Asp	Asn	Leu	His	Ser	Pro	Leu	Leu	Ser	Arg	Gln	Ala	Thr	Gly	Ala
195		370					375					380				
196	Glu	Gly	Lys	Asp	Ile	Val	His	His	Gly	His	Arg	Gly	Ser	Ala	Leu	Ser
197		385					390					395				400
198	Met	Arg	Arg	Gln	Ser	Leu	Leu	Gly	Glu	Gly	Gly	Asp	Gly	Val	Ser	Ser
199					405						410					415
200	Thr	Asp	Ile	Gly	Gly	Gly	Trp	Gln	Leu	Ala	Trp	Lys	Trp	Ser	Glu	Lys
201				420					425					430		
202	Glu	Gly	Glu	Asn	Gly	Arg	Lys	Glu	Gly	Gly	Phe	Lys	Arg	Val	Tyr	Leu
203			435					440					445			
204	His	Gln	Glu	Gly	Val	Pro	Gly	Ser	Arg	Arg	Gly	Ser	Ile	Val	Ser	Leu
205		450					455					460				
206	Pro	Gly	Gly	Gly	Asp	Val	Leu	Glu	Gly	Ser	Glu	Phe	Val	His	Ala	Ala
207		465				470					475					480
208	Ala	Leu	Val	Ser	Gln	Ser	Ala	Leu	Phe	Ser	Lys	Gly	Leu	Ala	Glu	Pro
209					485						490					495
210	Arg	Met	Ser	Asp	Ala	Ala	Met	Val	His	Pro	Ser	Glu	Val	Ala	Ala	Lys
211				500					505					510		
212	Gly	Ser	Arg	Trp	Lys	Asp	Leu	Phe	Glu	Pro	Gly	Val	Arg	Arg	Ala	Leu
213			515					520					525			
214	Leu	Val	Gly	Val	Gly	Ile	Gln	Ile	Leu	Gln	Gln	Phe	Ala	Gly	Ile	Asn
215		530					535					540				
216	Gly	Val	Leu	Tyr	Tyr	Thr	Pro	Gln	Ile	Leu	Glu	Gln	Ala	Gly	Val	Ala
217		545				550					555					560
218	Val	Ile	Leu	Ser	Lys	Phe	Gly	Leu	Ser	Ser	Ala	Ser	Ala	Ser	Ile	Leu
219					565					570					575	
220	Ile	Ser	Ser	Leu	Thr	Thr	Leu	Leu	Met	Leu	Pro	Cys	Ile	Gly	Phe	Ala
221				580					585					590		
222	Met	Leu	Leu	Met	Asp	Leu	Ser	Gly	Arg	Arg	Phe	Leu	Leu	Leu	Gly	Thr
223			595					600					605			
224	Ile	Pro	Ile	Leu	Ile	Ala	Ser	Leu	Val	Ile	Leu	Val	Val	Ser	Asn	Leu
225		610					615					620				
226	Ile	Asp	Leu	Gly	Thr	Leu	Ala	His	Ala	Leu	Leu	Ser	Thr	Ile	Ser	Val
227		625				630					635					640
228	Ile	Val	Tyr	Phe	Cys	Cys	Phe	Val	Met	Gly	Phe	Gly	Pro	Ile	Pro	Asn
229					645					650					655	
230	Ile	Leu	Cys	Ala	Glu	Ile	Phe	Pro	Thr	Arg	Val	Arg	Gly	Leu	Cys	Ile
231				660					665					670		
232	Ala	Ile	Cys	Ala	Phe	Thr	Phe	Trp	Ile	Gly	Asp	Ile	Ile	Val	Thr	Tyr
233			675													

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/051,902A

DATE: 08/23/2004
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Input Set : N:\AMC\US10051902A.raw
Output Set: N:\CRF4\08232004\J051902A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 29,622,636,638,669,771,822,856,889,896,944

Seq#:2; Xaa Pos. 129,133,134,144,178,207,218,220,236

Seq#:3; N Pos. 193,388,435,439

Seq#:4; Xaa Pos. 65,130

Seq#:11; N Pos. 421,434,441,458,483,493,498

Seq#:17; N Pos. 149,271,304,334,357,476,599,602

Seq#:18; Xaa Pos. 34,85,98,112,151

Seq#:22; Xaa Pos. 102

VERIFICATION SUMMARY

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Input Set : N:\AMC\US10051902A.raw

Output Set: N:\CRF4\08232004\J051902A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:128
M:341 Repeated in SeqNo=2
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180
M:341 Repeated in SeqNo=3
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:64
M:341 Repeated in SeqNo=4
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:420
M:341 Repeated in SeqNo=11
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:120
M:341 Repeated in SeqNo=17
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:32
M:341 Repeated in SeqNo=18
L:1074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:96